Striped bass (*Morone saxatilis*) are a long-lived anadromous fish of the U.S. mid-Atlantic. The species experienced a steep decline in the 1980s and the 1984 Atlantic Striped Bass Conservation Act became U.S. law with a goal to recover the species from low population sizes. While now considered demographically recovered, little is known about any population genetic impacts of the population decline and recovery. We tested the hypothesis that the precipitous decline and subsequent recovery of $N_C$ reduced $N_b$ and the ratio of genetic-to-census size ($N_b/N_C$).

Approximately 100 striped bass (*Morone saxatilis*) from each of 1970, 1978, 1986 and 1991 cohorts in archived scales as well as young-of-the-year for 1999 and 2006 cohorts were genotyped at seven to 17 loci microsatellite loci. Estimates of $N_b$ based on genetic association between pairs of loci and two-sample temporal methods were in the tens to low thousands in the recent past and remained approximately constant since 1970. Longer-term estimates of $N_e$ made via coalescent estimates of the effective mutation rate ($4N_e\mu$) were of order thousand to ten thousand and larger than $N_b$ in the recent past. $N_b/N_C$ was of order $1 \times 10^{-5}$ based on genetic association and temporal estimates of $N_b$, showing that genetic drift was strong despite large census size. The 1980s $N_C$ decline was not a marked genetic bottleneck, with no impact on allelic richness or $N_b$ given confidence intervals, partly because $N_b$ was consistently low across the entire time period. Despite a demographic recovery, low $N_b$ and $N_b/N_C$ highlight the need to monitor population genetic parameters in this species.